Sequence Range: 1 to 6200

```
        10         20         30         40         50         60         70
GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT

        80         90        100        110        120        130        140
AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA

       150        160        170        180        190        200        210
ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG

       220        230        240        250        260        270        280
ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC

       290        300        310        320        330        340        350
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG

       360        370        380        390        400        410        420
CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC

       430        440        450        460        470        480        490
ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC

       500        510        520        530        540        550        560
AAGTACGCCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA

       570        580        590        600        610        620        630
TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC

       640        650        660        670        680        690        700
AGTACATCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA

       710        720        730        740        750        760        770
TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG

       780        790        800        810        820        830        840
CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA

       850        860        870        880        890        900        910
CTGCTTAACT GGCTTATCGA AATTAATACG ACTCACTATA GGGAGACCCA AGCTTCGCAG AATTCCTGCG

       920        930        940        950        960        970        980
GCTGCTACAG TGTGTCCAGC GTCCTGCCTG GCTGTGCTGA GCGCTGGAAC AGTGGCGCAT CATTCAAGTG

       990       1000       1010       1020       1030       1040       1050
CACAGTTACC CATCCTGAGT CTGGCACCTT AACTGGCACA ATTGCCAAAG TCACAGGTGA GCTCAGATGC
```


FIGURE 1

Homo sapiens

```
      1060        1070        1080        1090        1100        1110        1120
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ATACCAGGAC ATTGTATGAC GTTCCCTGCT CACATGCCTG CTTTCTTCCT ATAATACAGA TGCTCAACTA

      1130        1140        1150        1160        1170        1180        1190
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ACTGCTCATG TCCTTATATC ACAGAGGGAA ATTGGAGCTA TCTGAGGAAC TGCCCAGAAG GGAAGGGCAG

      1200        1210        1220        1230        1240        1250        1260
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
AGGGGTCTTG CTCTCCTTGT CTGAGCCATA ACTCTTCTTT CTACCTTCCA GTGAACACCT TCCCACCCCA

      1270        1280        1290        1300        1310        1320        1330
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GGTCCACCTG CTACCGCCGC CGTCGGAGGA GCTGGCCCTG AATGAGCTCT TGTCCCTGAC ATGCCTGGTG

      1340        1350        1360        1370        1380        1390        1400
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CGAGCTTTCA ACCCTAAAGA AGTGCTGGTG CGATGGCTGC ATGGAAATGA GGAGCTGTCC CCAGAAAGCT

      1410        1420        1430        1440        1450        1460        1470
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
ACCTAGTGTT TGAGCCCCTA AAGGAGCCAG GCGAGGGAGC CACCACCTAC CTGGTGACAA GCGTGTTGCG

      1480        1490        1500        1510        1520        1530        1540
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TGTATCAGCT GAAAGCTTGA TATCGAATTC CGGAGGCGGA ACCGGCAGTG CAGCCCGAAG CCCCGCAGTC

      1550        1560        1570        1580        1590
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CCCGAGCACG CGTGGCC ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG
                   Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu>
                    ___a___a___a___a___a__ORF RF[1] ___a___a___a___a___a___>

1600        1610        1620        1630        1640        1650
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCC CCG CAC CTG GTG CAT
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

      1660        1670        1680        1690        1700        1710
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

      1720        1730        1740        1750        1760        1770
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

      1780        1790        1800        1810        1820
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

1830        1840        1850        1860        1870        1880
  *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr>
```

FIGURE 1A

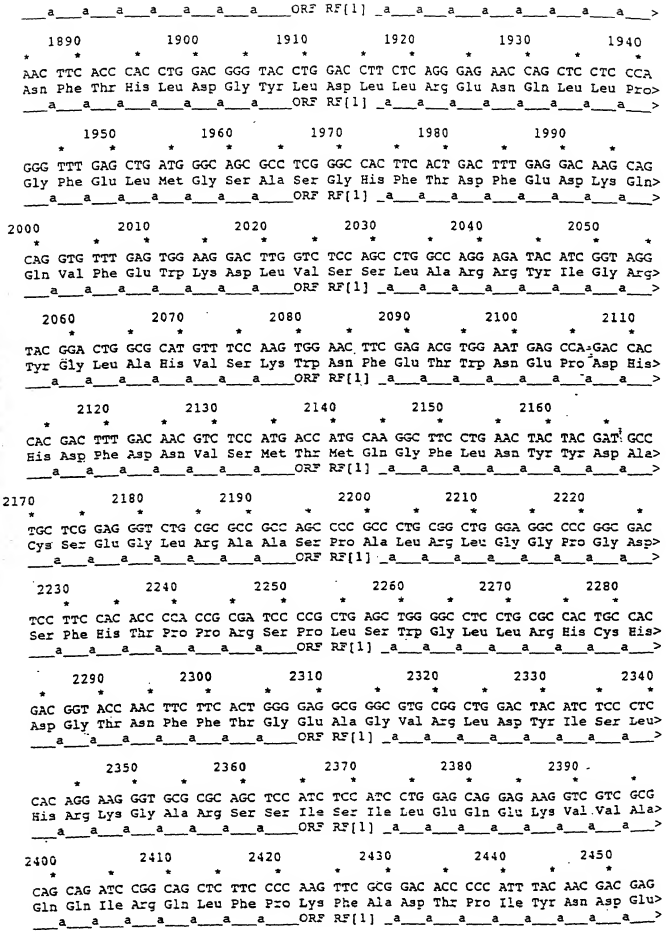


FIGURE 1B

```
  2460        2470       2480       2490        2500       2510
*    *    *    *    *    *    *    *    *    *    *    *
GCG GAC CCG CTG GTG GGC TGG TCC CTG CCA CAG CCG TGG AGG GCG GAC GTG ACC TAC
Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

     2520       2530       2540       2550       2560
   *    *    *    *    *    *    *    *    *    *    *
GCG GCC ATG GTG GTG AAG GTC ATC GCG CAG CAT CAG AAC CTG CTA CTG GCC AAC ACC
Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

2570       2580       2590       2600       2610       2620
 *    *    *    *    *    *    *    *    *    *    *    *
ACC TCC GCC TTC CCC TAC GCG CTC CTG AGC AAC GAC AAT GCC TTC CTG AGC TAC CAC
Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

  2630       2640       2650       2660       2670       2680
    *    *    *    *    *    *    *    *    *    *    *
CCG CAC CCC TTC GCG CAG CGC ACG CTC ACC GCG CGC TTC CAG GTC AAC AAC ACC CGC
Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

     2690       2700       2710       2720       2730
 *    *    *    *    *    *    *    *    *    *    *
CCG CCG CAC GTG CAG CTG TTG CGC AAG CCG GTG CTC ACG GCC ATG GGG CTG CTG GCG
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

2740       2750       2760       2770       2780       2790
 *    *    *    *    *    *    *    *    *    *    *    *
CTG CTG GAT GAG GAG CAG CTC TGG GCC GAA GTG TCG CAG GCC GGG ACC GTC CTG GAC
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

  2800       2810       2820       2830       2840       2850
    *    *    *    *    *    *    *    *    *    *    *
AGC AAC CAC ACG GTG GGC GTC CTG GCC AGC GCC CAC CGC CCC CAG GGC CCG GCC GAC
Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

     2860       2870       2880       2890       2900       2910
 *    *    *    *    *    *    *    *    *    *    *    *
GCC TGG CGC GCC GCG GTG CTG ATC TAC GCG AGC GAC GAC ACC CGC GCC CAC CCC AAC
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

     2920       2930       2940       2950       2960
   *    *    *    *    *    *    *    *    *    *    *
CGC AGC GTC GCG GTG ACC CTG CGG CTG CGC GGG GTG CCC CCC GGC CCG GGC CTG GTC
Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

2970       2980       2990       3000       3010       3020
 *    *    *    *    *    *    *    *    *    *    *
TAC GTC ACG CGC TAC CTG GAC AAC GGG CTC TGC AGC CCC GAC GGC GAG TGG CGG CGC
Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

  3030       3040       3050       3060       3070       3080
*    *    *    *    *    *    *    *    *    *    *    *
```

FIGURE 1C

```
CTG GGC CGG CCC GTC TTC CCC ACG GCA GAG CAG TTC CGG CGC ATG CGC GCG GCT GAG
Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

        3090          3100          3110          3120          3130
      *     *       *     *       *     *       *     *       *     *
GAC CCG GTG GCC GCG GCG CCC CGC CCC TTA CCC GCC GGC GGC CGC CTG ACC CTG CGC
Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

3140          3150          3160          3170          3180          3190
  *     *       *     *       *     *       *     *       *     *       *
CCC GCG CTG CGG CTG CCG TCG CTT TTG CTG GTG CAC GTG TGT GCG CGC CCC GAG AAG
Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

    3200          3210          3220          3230          3240          3250
  *     *       *     *       *     *       *     *       *     *       *     *
CCG CCC GGG CAG GTC ACG CGG CTC CGC GCC CTG CCC CTG ACC CAA GGG CAG CTG GTT
Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln Leu Val>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

      3260          3270          3280          3290          3300
    *     *       *     *       *     *       *     *       *     *
CTG GTC TGG TCG GAT GAA CAC GTG GGC TCC AAG TGC CTG TGG ACA TAC GAG ATC CAG
Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr Tyr Glu Ile Gln>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

3310          3320          3330          3340          3350          3360
  *     *       *     *       *     *       *     *       *     *       *
TTC TCT CAG GAC GGT AAG GCG TAC ACC CCG GTC AGC AGG AAG CCA TCG ACC TTC AAC
Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

    3370          3380          3390          3400          3410          3420
  *     *       *     *       *     *       *     *       *     *       *     *
CTC TTT GTG TTC AGC CCA GAC ACA GGT GCT GTC TCT GGC TCC TAC CGA GTT CGA GCC
Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

      3430          3440          3450          3460          3470          3480
    *     *       *     *       *     *       *     *       *     *       *     *
CTG GAC TAC TGG GCC CGA CCA GGC CCC TTC TCG GAC CCT GTG CCG TAC CTG GAG GTC
Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val>
___a___a___a___a___a___a___a____ORF RF[1] _a___a___a___a___a___a___a___a___>

        3490          3500          3510          3520          3530          3540
      *     *       *     *       *     *       *     *       *     *       *     *
CCT GTG CCA AGA GGG CCC CCA TCC CCG GGC AAT CCA TGAG CCTGTGCTGA GCCCCAGTGG
Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro>
___a___a___a__ORF RF[1] ___a___a___a___>

      3550          3560          3570          3580          3590          3600          3610
    *     *       *     *       *     *       *     *       *     *       *     *       *     *
GTTGCACCTC CACCGGCAGT CAGCGAGCTG GGGCTGCACT GTGCCCATGC TGCCCTCCCA TCACCCCCTT

      3620          3630          3640          3650          3660          3670          3680
    *     *       *     *       *     *       *     *       *     *       *     *       *     *
TGCAATATAT TTTTATATTT TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

      3690          3700          3710          3720          3730          3740          3750
    *     *       *     *       *     *       *     *       *     *       *     *       *     *
```

FIGURE 1D

```
AAAAAAAAAA AAAAAAAAAG AATTCCTGCA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTTAAACC

      3760       3770       3780       3790       3800       3810       3820
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT

      3830       3840       3850       3860       3870       3880       3890
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
TGACCCTGGA AGGTGCCACT CCCACTGTCC TTTCCTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG

      3900       3910       3920       3930       3940       3950       3960
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC

      3970       3980       3990       4000       4010       4020       4030
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGAGCTT

      4040       4050       4060       4070       4080       4090       4100
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA

      4110       4120       4130       4140       4150       4160       4170
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCGCT

      4180       4190       4200       4210       4220       4230       4240
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG

      4250       4260       4270       4280       4290       4300       4310
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC TGCGCTCGGT CGTTCGGCTG

      4320       4330       4340       4350       4360       4370       4380
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA

      4390       4400       4410       4420       4430       4440       4450
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA

      4460       4470       4480       4490       4500       4510       4520
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA

      4530       4540       4550       4560       4570       4580       4590
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA

      4600       4610       4620       4630       4640       4650       4660
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCACGCT GTAGGTATCT

      4670       4680       4690       4700       4710       4720       4730
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC

      4740       4750       4760       4770       4780       4790       4800
      *  *       *  *       *  *       *  *       *  *       *  *       *  *
GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA
```

FIGURE 1E

4810 4820 4830 4840 4850 4860 4870

CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA

4880 4890 4900 4910 4920 4930 4940

CGGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT

4950 4960 4970 4980 4990 5000 5010

GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA

5020 5030 5040 5050 5060 5070 5080

CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA

5090 5100 5110 5120 5130 5140 5150

AAACTCACGT TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTAAATTAA

5160 5170 5180 5190 5200 5210 5220

AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA CTTGGTCTGA CAGTTACCAA TGCTTAATCA

5230 5240 5250 5260 5270 5280 5290

GTGAGGCACC TATCTCAGCG ATCTGTCTAT TTCGTTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT

5300 5310 5320 5330 5340 5350 5360

AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG

5370 5380 5390 5400 5410 5420 5430

GCTCCAGATT TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT GCAACTTTAT

5440 5450 5460 5470 5480 5490 5500

CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGCG

5510 5520 5530 5540 5550 5560 5570

CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC

5580 5590 5600 5610 5620 5630 5640

GGTTCCCAAC GATCAAGGCG AGTTACATGA TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC

5650 5660 5670 5680 5690 5700 5710

CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTTATC ACTCATGGTT ATGGCAGCAC TGCATAATTC

5720 5730 5740 5750 5760 5770 5780

TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA

5790 5800 5810 5820 5830 5840 5850

TAGTGTATGC GGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA CATAGCAGAA

5860 5870 5880 5890 5900 5910 5920

FIGURE 1F

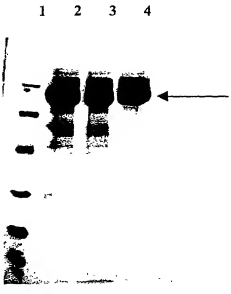
```
CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG

      5930       5940       5950       5960       5970       5980       5990
     *    *     *    *     *    *     *    *     *    *     *    *     *    *
ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTCAC CAGCGTTTCT

      6000       6010       6020       6030       6040       6050       6060
     *    *     *    *     *    *     *    *     *    *     *    *     *    *
GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG GAATAAGGGC GACACGGAAA TGTTGAATAC

      6070       6080       6090       6100       6110       6120       6130
     *    *     *    *     *    *     *    *     *    *     *    *     *    *
TCATACTCTT CCTTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT

      6140       6150       6160       6170       6180       6190       6200
     *    *     *    *     *    *     *    *     *    *     *    *     *    *
TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC
```

FIGURE 1G

FIGURE 2. SDS-POLYACRYLAMIDE GELS DEMONSTRATING IMPROVEMENTS IN PURITY

Gel using the Kakkis et al 1994, published procedure for purification

Gel using the new Galli Process contained in this application



1. Molecular Weight Marker
2. Prior Process Carson (nonpublished) Batch 2000C9001 Reference Reduced (7.5 µg)
3. Same Batch 2000C9001 Reference Reduced (5.0 µg)
4. Galli Process Enzyme Batch P10006 (5.0 µg)

FIGURE 2

FIGURE 3A IDURONIDASE PRODUCTION USING THE GALLI PROCESS

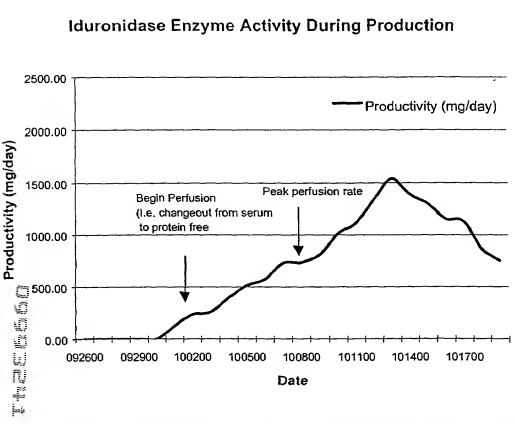
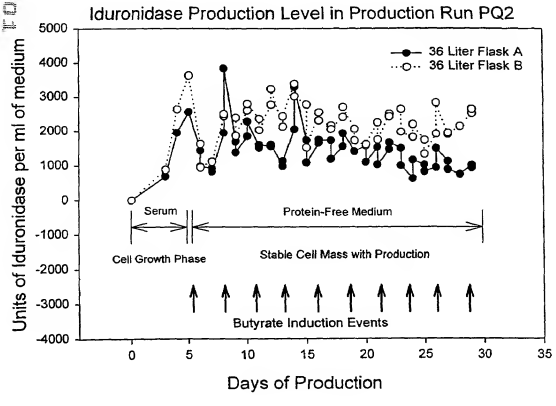
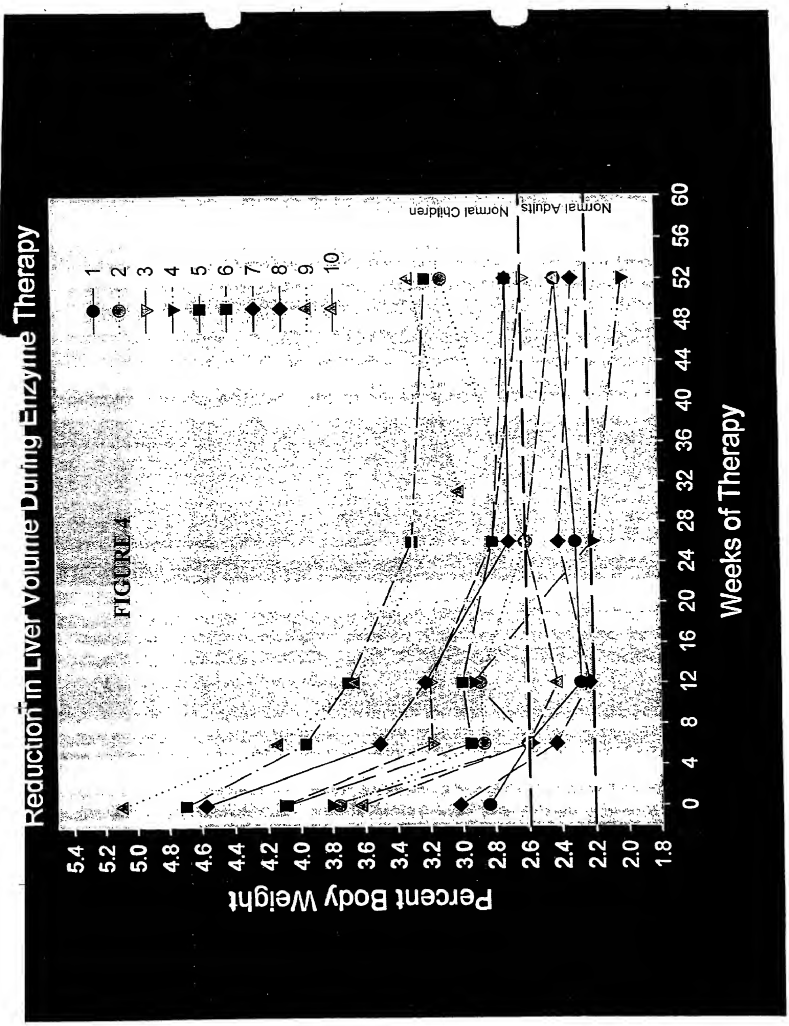


FIGURE 3B. IDURONIDASE PRODUCTION USING BUTYRATE INDUCTION





Reduction in Liver Volume During Enzyme Therapy
FIGURE 4
Percent Body Weight
5.4
5.2
5.0
4.8
4.6
4.4
4.2
4.0
3.8
3.6
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
1.8
Weeks of Therapy
0
4
8
12
16
20
24
28
32
36
40
44
48
52
56
60
1
2
3
4
5
6
7
8
9
10
Normal Children
Normal Adults

FIGURE 4

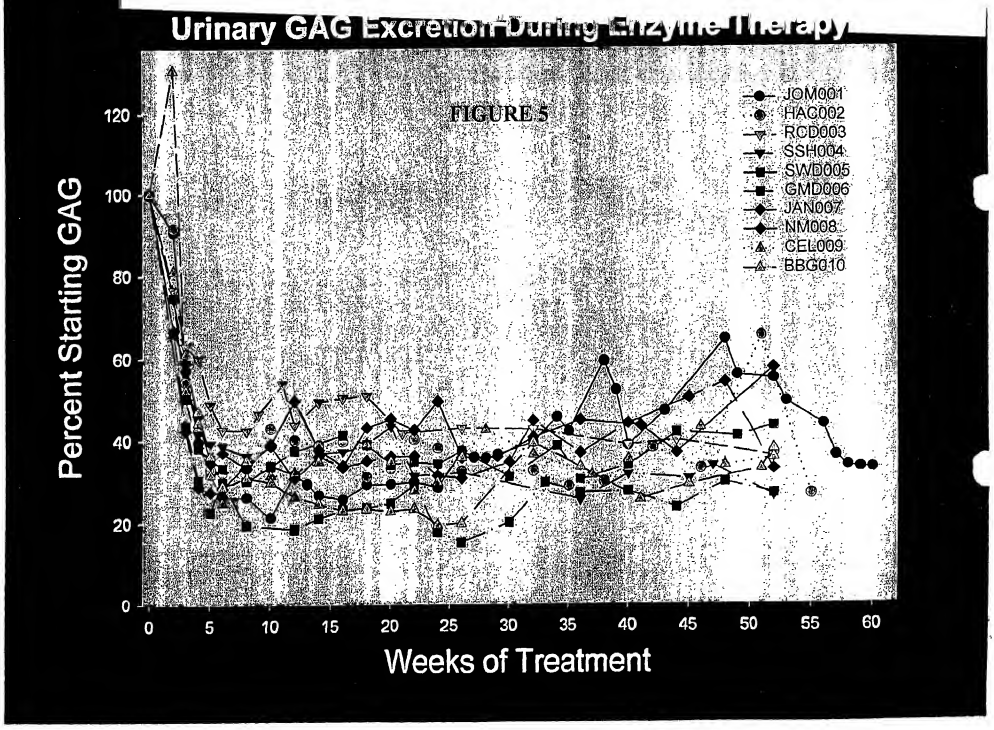

Urinary GAG Excretion During Enzyme Therapy
FIGURE 5
Percent Starting GAG
Weeks of Treatment
0
20
40
60
80
100
120
0
5
10
15
20
25
30
35
40
45
50
55
60
JOM001
HAC002
RCD003
SSH004
SWD005
GMD006
JAN007
NM008
CEL009
BBG010

FIGURE 5

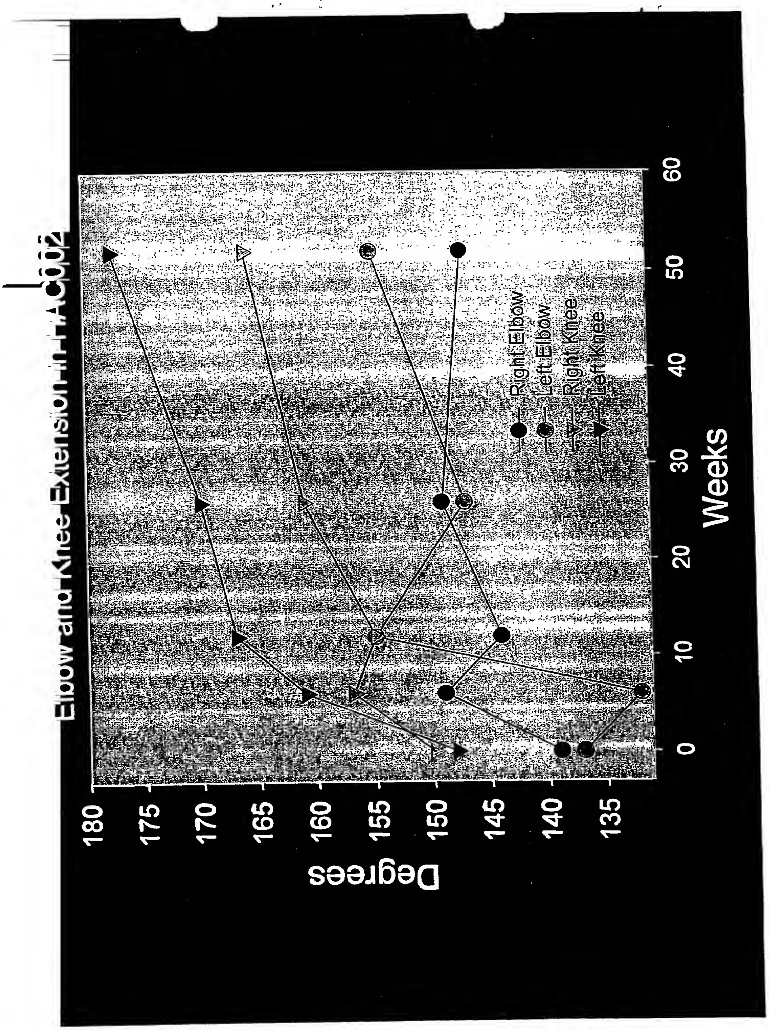

Elbow and Knee Extension in
Degrees
180
175
170
165
160
155
150
145
140
135
Weeks
0
10
20
30
40
50
60
Right Elbow
Left Elbow
Right Knee
Left Knee

FIGURE 6

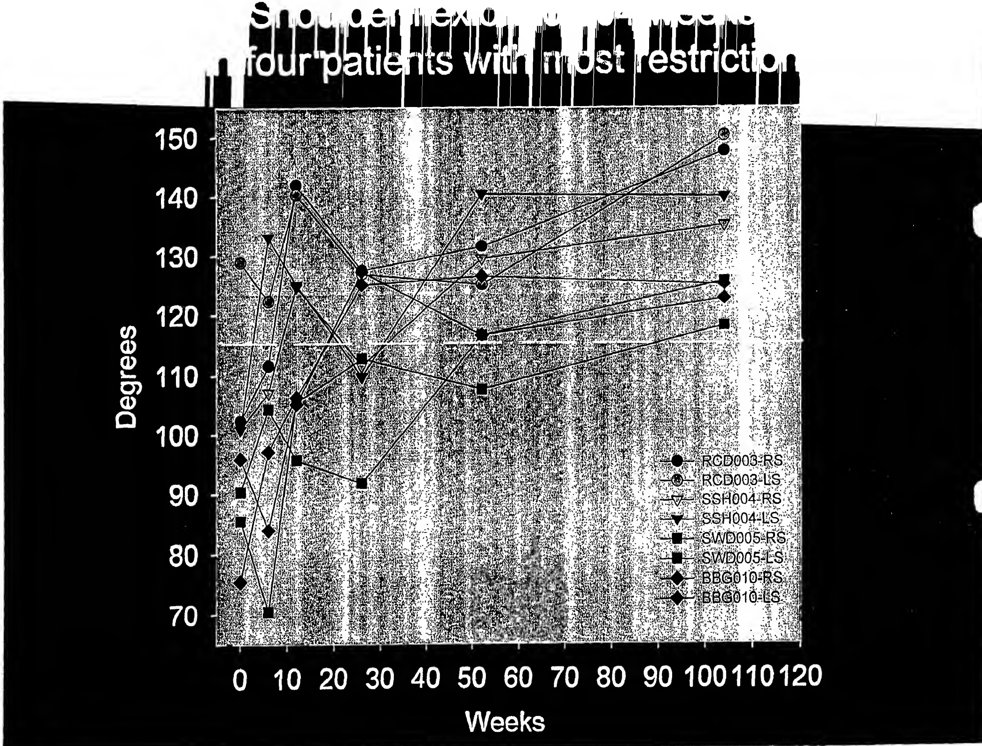

four patients with
Degrees
150
140
130
120
110
100
90
80
70
0 10 20 30 40 50 60 70 80 90 100 110 120
Weeks
RCD003-RS
RCD003-LS
SSH004-RS
SSH004-LS
SWD005-RS
SWD005-LS
BBG010-RS
BBG010-LS

FIGURE 7

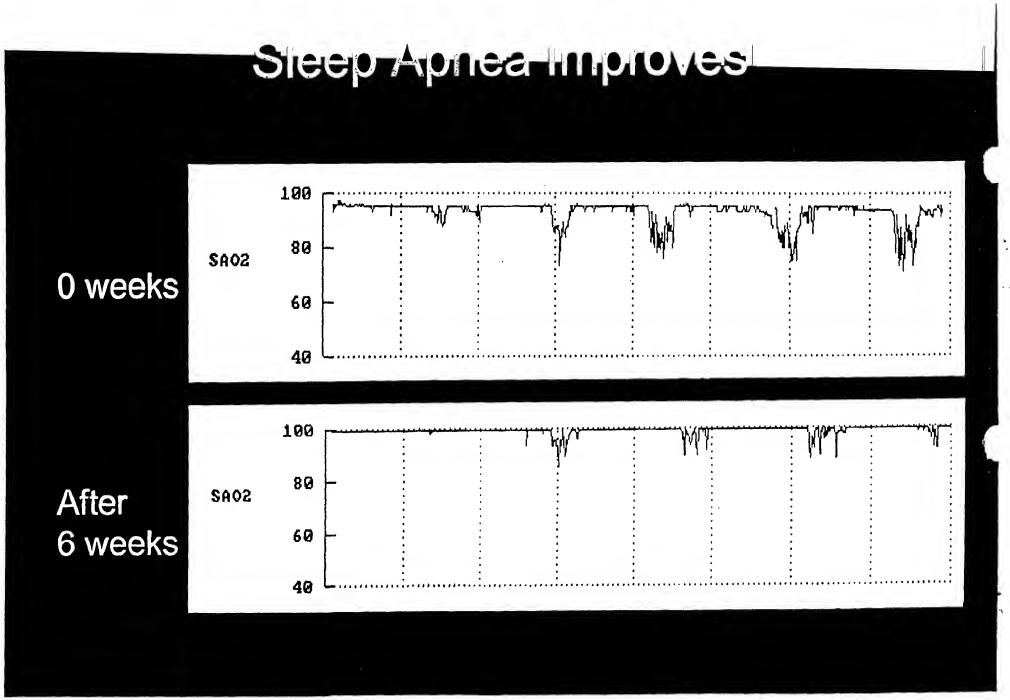
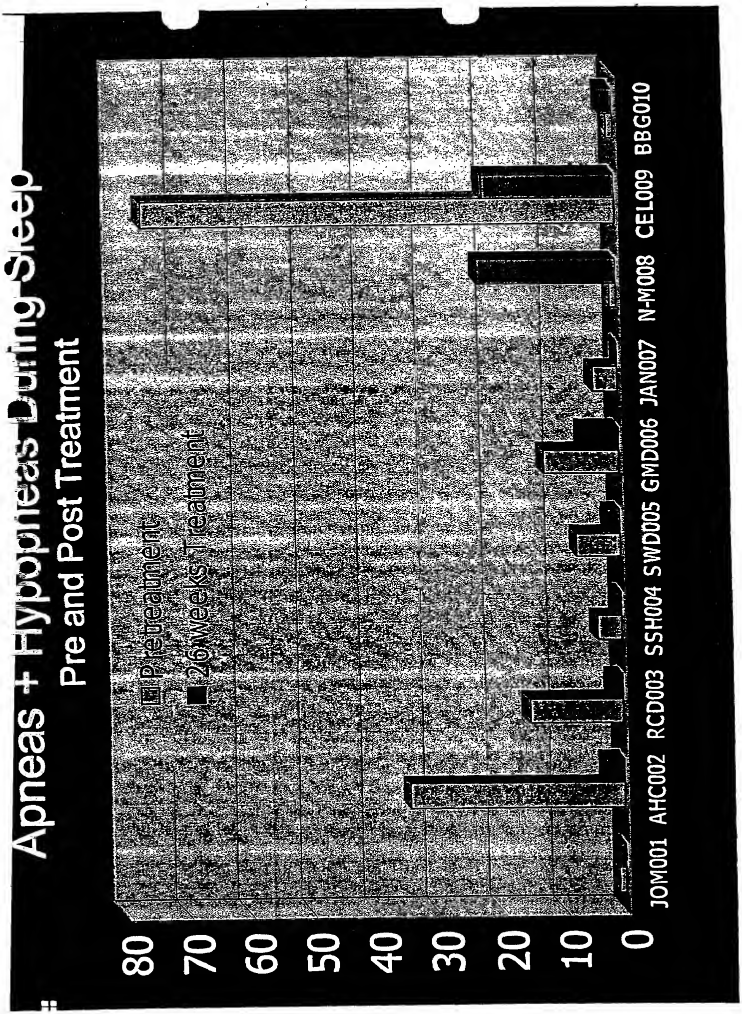

Sleep Apnea Improves
0 weeks
SAO2
100
80
60
40
After
6 weeks
SAO2
100
80
60
40

FIGURE 8



Apneas + Hypopneas During Sleep
Pre and Post Treatment
Pretreatment
26 weeks Treatment
80
70
60
50
40
30
20
10
0
JOM001
AHC002
RCD003
SSH004
SWD005
GMD006
JAN007
N-M008
CEL009
BBG010

FIGURE 9

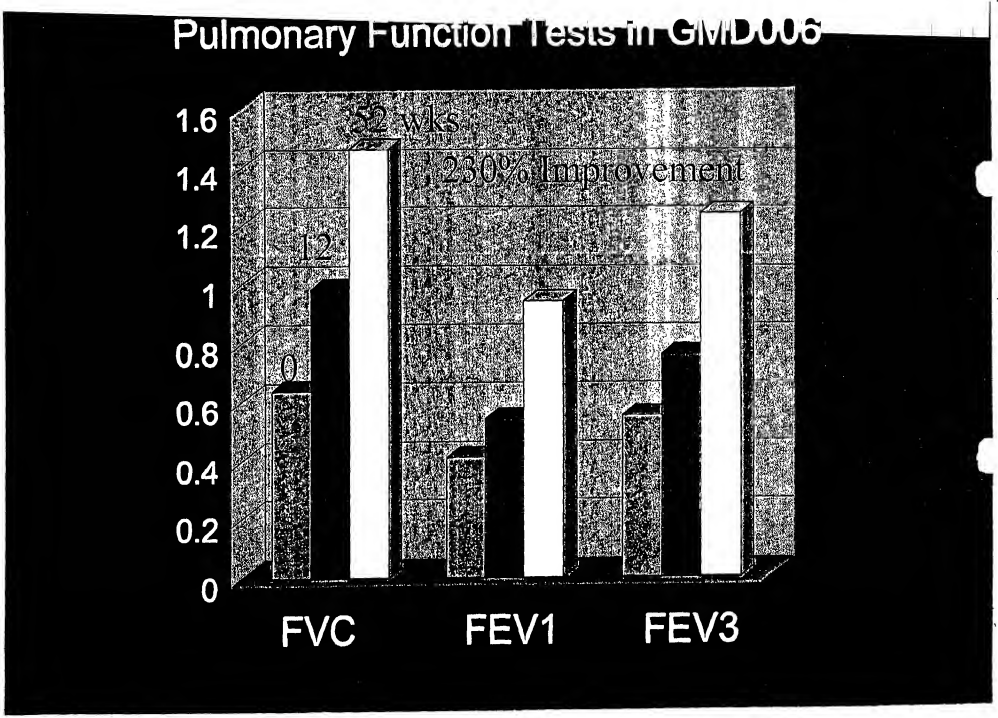
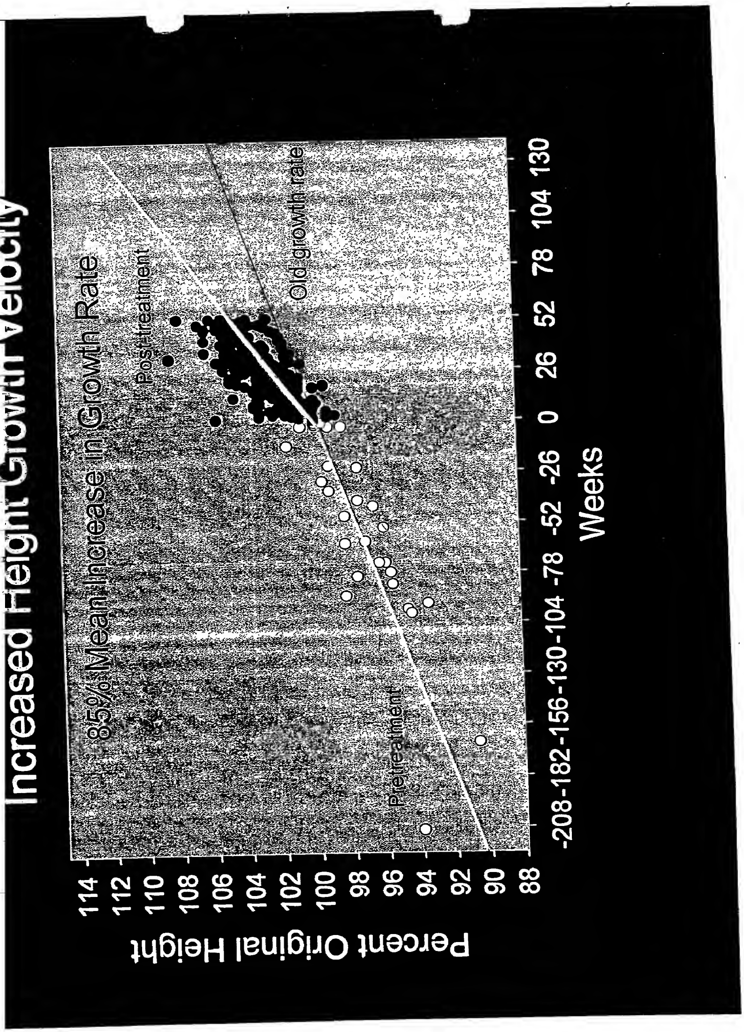

Pulmonary Function Tests in GMD006
52 wks
230% Improvement
12
0
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
FVC
FEV1
FEV3

FIGURE 10



Increased Height Growth Velocity
85% Mean Increase in Growth Rate
Post-treatment
Old growth rate
Pretreatment
Percent Original Height
114
112
110
108
106
104
102
100
98
96
94
92
90
88
Weeks
-208
-182
-156
-130
-104
-78
-52
-26
0
26
52
78
104
130

FIGURE 11

FIGURE 12.

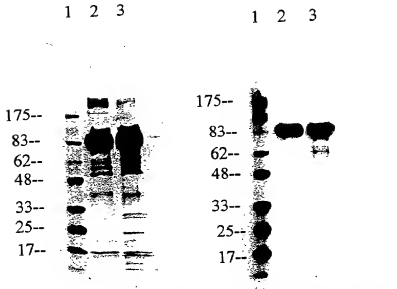
COMPARISON OF HOST PROTEIN CONTAMINATION BETWEEN A PRIOR AND THE NEW GALLI PROCESS

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

FIGURE 12

Comparison of Galli and Carson Material



anit-IDU Western blot 1:50,000

SDS-PAGE silver stain

1 Marker
2 Galli Referenced-0201
3 Carson C9002

5ug/lane

FIGURE 13